



IFWO

RAW SEQUENCE LISTING

DATE: 07/30/2004

PATENT APPLICATION: US/10/670,454

TIME: 14:14:37

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1 <110> APPLICANT: Thomas, Stephen G
 2 Hedden, Peter
 3 Phillips, Andrew L
 4 <120> TITLE OF INVENTION: Gibberellin 2-Oxidase
 5 <130> FILE REFERENCE: 0623.0970000
 6 <140> CURRENT APPLICATION NUMBER: US/10/670,454
 7 <141> CURRENT FILING DATE: 2003-09-26
 8 <150> PRIOR APPLICATION NUMBER: US/09/719,108
 9 <151> PRIOR FILING DATE: 2000-12-08
 10 <150> PRIOR APPLICATION NUMBER: PCT/GB99/01857
 11 <151> PRIOR FILING DATE: 1999-06-11
 12 <150> PRIOR APPLICATION NUMBER: GB 9812821.8
 13 <151> PRIOR FILING DATE: 1998-06-12
 14 <150> PRIOR APPLICATION NUMBER: GB 9815404.0
 15 <151> PRIOR FILING DATE: 1998-07-15
 16 <160> NUMBER OF SEQ ID NOS: 16
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1318
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Phaseolus coccineus
 23 <400> SEQUENCE: 1

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 26 caagtccacg cccttggtca cggggattcc tgtggtcgac ctcacgcacc ccgatgccaa 180
 27 gaattctcata gtgaacgcct gtagggactt cggcttcttc aagcttgtga accatgggtg 240
 28 tccattggag ttaatggcca atttagaaaa cgaggccctc aggttcttta aaaaatctca 300
 29 gtccgagaaa gacagagctg gtcccccgga ccctttcggc tatggtagca agaggattgg 360
 30 cccaaacggt gatgtcgggt gggtcgaata cctcctctc aacaccaacc ctgatgttat 420
 31 ctcacccaaa tcactttgca ttttcgaga aaatcctcat catttcaggg cgggtggtgga 480
 32 gaactacatt acagcagtga agaacatgtg ctatgcgggt ttggaattga tggcggaggg 540
 33 gttggggata aggcagagga atacgttaag caggttgctg aaggatgaga aaagtgattc 600
 34 gtgcttcagg ttgaaccact accgccttg ccctgaggtg caagcactga accggaattt 660
 35 gggtgggttt ggggagcaca cagaccaca gataatttct gtcttaagat ctaacagcac 720
 36 atctggcttg caaatctgtc tcacagatgg cacttgggtt tcagtccac ctgatcagac 780
 37 ttcctttttc atcaatgttg gtgacgctct acaggtaatg actaatggga ggtttaaaag 840
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 39 aggaccagcg ttgagtgaat atatagcacc tttaccttca gtgatgttaa aaggagagga 960
 40 gtgtttgtac aaagagttca catggtgtga atacaagaag gctgcgtaca cttcaaggct 1020
 41 agctgataat aggccttgccc ctttcagaa atctgctgct gattaaccaa acacaccctt 1080
 42 caaattccac tcaattttac cacgtgttat taccccaatt ttctttcctt tttcttttcc 1140
 43 tgtgtctgtc taggtttcaa acagttgact ctacttgaca tatatagaaa atgaataggt 1200
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49 <212> TYPE: PRT
50 <213> ORGANISM: Phaseolus coccineus
51 <400> SEQUENCE: 2
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55          20              25              30
56      Thr His Pro Asp Ala Lys Asn Leu Ile Val Asn Ala Cys Arg Asp Phe
57          35              40              45
58      Gly Phe Phe Lys Leu Val Asn His Gly Val Pro Leu Glu Leu Met Ala
59          50              55              60
60      Asn Leu Glu Asn Glu Ala Leu Arg Phe Phe Lys Lys Ser Gln Ser Glu
61          65              70              75              80
62      Lys Asp Arg Ala Gly Pro Pro Asp Pro Phe Gly Tyr Gly Ser Lys Arg
63          85              90              95
64      Ile Gly Pro Asn Gly Asp Val Gly Trp Val Glu Tyr Leu Leu Leu Asn
65          100             105             110
66      Thr Asn Pro Asp Val Ile Ser Pro Lys Ser Leu Cys Ile Phe Arg Glu
67          115             120             125
68      Asn Pro His His Phe Arg Ala Val Val Glu Asn Tyr Ile Thr Ala Val
69          130             135             140
70      Lys Asn Met Cys Tyr Ala Val Leu Glu Leu Met Ala Glu Gly Leu Gly
71          145             150             155             160
72      Ile Arg Gln Arg Asn Thr Leu Ser Arg Leu Leu Lys Asp Glu Lys Ser
73          165             170             175
74      Asp Ser Cys Phe Arg Leu Asn His Tyr Pro Pro Cys Pro Glu Val Gln
75          180             185             190
76      Ala Leu Asn Arg Asn Leu Val Gly Phe Gly Glu His Thr Asp Pro Gln
77          195             200             205
78      Ile Ile Ser Val Leu Arg Ser Asn Ser Thr Ser Gly Leu Gln Ile Cys
79          210             215             220
80      Leu Thr Asp Gly Thr Trp Val Ser Val Pro Pro Asp Gln Thr Ser Phe
81          225             230             235             240
82      Phe Ile Asn Val Gly Asp Ala Leu Gln Val Met Thr Asn Gly Arg Phe
83          245             250             255
84      Lys Ser Val Lys His Arg Val Leu Ala Asp Thr Thr Lys Ser Arg Leu
85          260             265             270
86      Ser Met Ile Tyr Phe Gly Gly Pro Ala Leu Ser Glu Asn Ile Ala Pro
87          275             280             285
88      Leu Pro Ser Val Met Leu Lys Gly Glu Glu Cys Leu Tyr Lys Glu Phe
89          290             295             300
90      Thr Trp Cys Glu Tyr Lys Lys Ala Ala Tyr Thr Ser Arg Leu Ala Asp
91          305             310             315             320
92      Asn Arg Leu Ala Pro Phe Gln Lys Ser Ala Ala
93          325             330
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96 <211> LENGTH: 210
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99 <220> FEATURE:
100 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
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103     tggtttttggg gaacacacag atcctcaaat catctctgtc ttaagatcta acaacacttc 120
104     tggctcccaa attaatctaa atgatggctc atggatctct gtccctcccg atcacacttc 180
105     cttcttcttc aacgtgggtg actctctcca                210
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109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
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115     atcgaggatt tcaatgatat atttcggcgg accgccattg agccagaaga tcgcaccatt 120
116     gccatgcctt gtccctgagc aagatgattg gctttacaaa gaattcactt ggtctcaata 180
117     caaatcttct gcttacaag                199
119 <210> SEQ ID NO: 5
120 <211> LENGTH: 1318
121 <212> TYPE: DNA
122 <213> ORGANISM: Arabidopsis thaliana
123 <220> FEATURE:
124 <221> NAME/KEY: misc_feature
125 <222> LOCATION: (1243, 1265)
126 <223> OTHER INFORMATION: unidentified residue
127 <400> SEQUENCE: 5
128     tcaaaatcaa aaaaattcta tcaacaagg aaatatatca atggcggtat tgtctaaacc 60
129     ggtagcaata ccaaaatccg ggttctctct aatcccgggt atagatatgt ctgaccacaga 120
130     atccaaacat gccctcgtga aagcatgcga agacttcggc ttcttcaagg tgatcaacca 180
131     tggcgtttcc gcagagctag tctctgtttt agaacacgag accgtcgatt tcttctcggt 240
132     gcccaagtca gagaaaaccc aagtcgcagg ttatcccttc ggatacggga acagtaagat 300
133     tggtcggaat ggtgacgtgg gttgggttga gtacttggtg atgaacgcta atcatgattc 360
134     cggttcgggt ccactatttc caagtcttct caaaagcccg ggaactttca gaaacgcatt 420
135     ggaagagtac acaacatcag tgagaaaaat gacattcgat gttttggaga agatcacaga 480
136     tgggctaggg atcaaaccga ggaacacact tagcaagctt gtgtctgacc aaaacacgga 540
137     ctcgatattg agacttaatc actatccacc atgtcctctt agcaataaga aaaccaatgg 600
138     tggtaagaat gtgattgggt ttggtgaaca cacagatcct caaatcatct ctgtcttaag 660
139     atctaacaac acttctgggt tccaaattaa tctaaatgat ggctcatgga tctctgtccc 720
140     tcccgatcac acttcttctt tcttcaacgt tggtgactct ctccagggtg tgacaaatgg 780
141     gaggttcaag agcgtgaggc atagggtttt agctaactgt aaaaaatcta ggggtttctat 840
142     gatttacttc gctggacctt cattgactca gagaatcgct ccgttgacat gtttgataga 900
143     caatgaggac gagaggttgt acgaggagtt tacttggtct gaatacaaaa actctacct 960
144     caactctaga ttgtctgata ataggcttca acaattcgaa aggaagacta taaaaaatct 1020
145     cctaaattga tgtgatatat ctattttaatc tataagtgtg tgctacatac agacaatgca 1080
146     tctgtatatt ttgaagtata atgttatttg ttaatccaat aactgtaaaa acatgcaaga 1140

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147      gtgtgtttgt ttgtttcgta atatcaacat cgtcccatc ttttatggat aaaaaaaaaa 1200
W--> 148      aaaaaaaaaa cactgttttg atgtaagcta cattttactt tangtgtaca tcttattgtg 1260
149      ttaantaaat tatttcaaaa taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1318
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152 <211> LENGTH: 329
153 <212> TYPE: PRT
154 <213> ORGANISM: Arabidopsis thaliana
155 <400> SEQUENCE: 6
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159      20          25          30
160      Val Lys Ala Cys Glu Asp Phe Gly Phe Phe Lys Val Ile Asn His Gly
161      35          40          45
162      Val Ser Ala Glu Leu Val Ser Val Leu Glu His Glu Thr Val Asp Phe
163      50          55          60
164      Phe Ser Leu Pro Lys Ser Glu Lys Thr Gln Val Ala Gly Tyr Pro Phe
165      65          70          75          80
166      Gly Tyr Gly Asn Ser Lys Ile Gly Arg Asn Gly Asp Val Gly Trp Val
167      85          90          95
168      Glu Tyr Leu Leu Met Asn Ala Asn His Asp Ser Gly Ser Gly Pro Leu
169      100         105         110
170      Phe Pro Ser Leu Leu Lys Ser Pro Gly Thr Phe Arg Asn Ala Leu Glu
171      115         120         125
172      Glu Tyr Thr Thr Ser Val Arg Lys Met Thr Phe Asp Val Leu Glu Lys
173      130         135         140
174      Ile Thr Asp Gly Leu Gly Ile Lys Pro Arg Asn Thr Leu Ser Lys Leu
175      145         150         155         160
176      Val Ser Asp Gln Asn Thr Asp Ser Ile Leu Arg Leu Asn His Tyr Pro
177      165         170         175
178      Pro Cys Pro Leu Ser Asn Lys Lys Thr Asn Gly Gly Lys Asn Val Ile
179      180         185         190
180      Gly Phe Gly Glu His Thr Asp Pro Gln Ile Ile Ser Val Leu Arg Ser
181      195         200         205
182      Asn Asn Thr Ser Gly Leu Gln Ile Asn Leu Asn Asp Gly Ser Trp Ile
183      210         215         220
184      Ser Val Pro Pro Asp His Thr Ser Phe Phe Phe Asn Val Gly Asp Ser
185      225         230         235         240
186      Leu Gln Val Met Thr Asn Gly Arg Phe Lys Ser Val Arg His Arg Val
187      245         250         255
188      Leu Ala Asn Cys Lys Lys Ser Arg Val Ser Met Ile Tyr Phe Ala Gly
189      260         265         270
190      Pro Ser Leu Thr Gln Arg Ile Ala Pro Leu Thr Cys Leu Ile Asp Asn
191      275         280         285
192      Glu Asp Glu Arg Leu Tyr Glu Glu Phe Thr Trp Ser Glu Tyr Lys Asn
193      290         295         300
194      Ser Thr Tyr Asn Ser Arg Leu Ser Asp Asn Arg Leu Gln Gln Phe Glu
195      305         310         315         320
196      Arg Lys Thr Ile Lys Asn Leu Leu Asn

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202 <213> ORGANISM: Arabidopsis thaliana
203 <400> SEQUENCE: 7
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206      ccacagccag tcactttaga taaccacatc tccctaatac ccacatacaa accggttccg 180
207      gttctcactt cccattcaat ccccgtcgtc aacctagccg atccggaagc gaaaaccgca 240
208      atcgtaaaag cctgcgagga gttcgggttc ttcaagggtc taaaccacgg agtccgaccc 300
209      gaactcatga ctcggttaga gcaggaggct attggcttct tcggcttgcc tcagtctctt 360
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211      ggtgacgttg gttggattga gtatctcttc ctcaatgcta atcctcagct ctctctctct 480
212      aaaacctccg ccgttttccg tcaaacccct caaattttcc gtgagtcggt ggaggagtac 540
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214      atagagccaa gggacactct gagtaaaatg ctgagagatg agaagagtga ctctgtcctg 660
215      agactaaacc attatccggc ggcggaggaa gaggcggaga agatggtgaa ggtgggggtt 720
216      ggggaacaca cagaccaca gataatctca gtgctaagat ctaataacac ggcgggtctt 780
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218      attaagtgtg gagatgctct tcaggttatg actaacggga ggttcaagag tggttaaacc 900
219      agggctcttag ccgatacaag gagatcgagg atttcaatga tatatttcgg cggaccgcca 960
220      ttgagccaga agatcgaccc attgccatgc ctgtccctg agcaagatga ttggctttac 1020
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222      agacttggtc tctttgagaa acaacctctt ctcaatcata aaaccttgt atgagagtag 1140
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228 <212> TYPE: PRT
229 <213> ORGANISM: Arabidopsis thaliana
230 <400> SEQUENCE: 8
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234      20 25 30
235      Val Val Asn Leu Ala Asp Pro Glu Ala Lys Thr Arg Ile Val Lys Ala
236      35 40 45
237      Cys Glu Glu Phe Gly Phe Phe Lys Val Val Asn His Gly Val Arg Pro
238      50 55 60
239      Glu Leu Met Thr Arg Leu Glu Gln Glu Ala Ile Gly Phe Phe Gly Leu
240      65 70 75 80
241      Pro Gln Ser Leu Lys Asn Arg Ala Gly Pro Pro Glu Pro Tyr Gly Tyr
242      85 90 95
243      Gly Asn Lys Arg Ile Gly Pro Asn Gly Asp Val Gly Trp Ile Glu Tyr
244      100 105 110
245      Leu Leu Leu Asn Ala Asn Pro Gln Leu Ser Ser Pro Lys Thr Ser Ala
246      115 120 125
247      Val Phe Arg Gln Thr Pro Gln Ile Phe Arg Glu Ser Val Glu Glu Tyr

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 1243,1265

VERIFICATION SUMMARY

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L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1200
M:341 Repeated in SeqNo=5